

AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1-13. (canceled)

14. (currently amended) A method for the production of L-amino acids using coryneform bacteria comprising:

a) fermenting coryneform bacteria which produce a desired L-amino acid comprising an overexpressed polynucleotide sigC wherein said polynucleotide comprises a nucleotide sequence of SEQ ID NO:1 and encodes a polypeptide having an RNA polymerase sigma C factor activity, wherein said overexpression is achieved by increasing the copy number of said polynucleotide or by operably linking said polynucleotide to a promoter.

15. (canceled)

16. (previously presented) The method according to claim 14, further comprising: isolating the L-amino acid.

17. (previously presented) The method according to claim 14, wherein the L amino acid is lysine.

18. (currently amended) A method for the production of L-amino acids using coryneform bacteria comprising:

fermenting coryneform bacteria which produce a desired L-amino acid comprising an overexpressed polynucleotide sigC wherein said polynucleotide encodes a polypeptide comprising an amino acid sequence of SEQ ID NO:2, wherein said overexpression is achieved by increasing the copy number of said polynucleotide.

- 19-20. (canceled)

21. (currently amended) The method according to claim 14, wherein ~~a strain transformed with a plasmid vector is used, and the plasmid vector carries the nucleotide sequence coding for the sigC gene~~ increasing the copy number is achieved by transforming said coryneform bacteria with a vector comprising said polynucleotide.

- 22-24. (canceled)

25. (currently amended) The method according to claim 14, wherein the bacteria being fermented comprise, at the same time, one or more genes which are overexpressed; wherein the one or more genes is/are selected from the group consisting of:

a gene dapA coding for dihydridipicolinate synthase,
a gene gap coding for glyceraldehyde-3-phosphate dehydrogenase,
a gene tpi coding for triosephosphate isomerase,
a gene pgk coding for 3-phosphoglycerate kinase,

a gene zwf coding for glucose-6-phosphate dehydrogenase,
a gene pye coding for pyruvate carboxylase,
a gene mqr coding for malate-quinone-oxidoreductase,
a gene lysC coding for a feedback resistant aspartate kinase,
~~gene lysE coding for a protein for lysine export,~~
a gene hom coding for homoserine dehydrogenase,
a gene ilvA coding for threonine dehydratase ~~or allele ilvA(Fbr) coding for a feedback resistant threonine dehydratase,~~
a gene ilvBN coding for acetohydroxy acid synthase,
a gene ilvD coding for dihydroxy acid dehydratase, and
a gene zwal coding for the a Zwa1 protein.

26. (currently amended) Process according to claim 14, wherein the bacteria being fermented comprise, at the same time, one or more genes which are eliminated; wherein the genes are selected from the group consisting of:

a gene pek coding for phosphoenol pyruvate carboxykinase,
a gene pgi coding for glucose-6-phosphate isomerase,
a gene poxB coding for pyruvate oxidase, ~~and~~
~~gene zwa2 coding for the Zwa2 protein.~~

27. (previously presented) The method according to claim 14 wherein the bacteria is *Corynebacterium glutamicum*.

28. (currently amended) The method according to claim 21 27, wherein the ~~Corynebacterium glutamicum is a said vector is pEC-XK99EsigCb2ex contained in Escherichia coli strain of DH5 α mcr/pEC-XK99EsigCb2ex deposited under DSM 14375.~~
29. (currently amended) ~~The method according to claim 27, wherein the Corynebacterium glutamicum is a strain of DSM5715/pEC-XK99E deposited under DSM 13455.~~
- 30-32. (canceled)
33. (new) The method according to claim 18 wherein said polynucleotide comprises nucleotides 300 to 878 of SEQ ID:1.
34. (new) A method for the production of L-amino acids using coryneform bacteria comprising:
fermenting coryneform bacteria which produce a desired L-amino acid comprising an overexpressed polynucleotide sigC wherein said polynucleotide comprises a nucleotide sequence of SEQ ID NO:1 and encodes a polypeptide having an RNA polymerase sigma-C factor.